

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 09:23:29 ; Search time 35.1849 seconds  
(without alignments)  
3900.178 Million cell updates/sec

Title: US-09-836-077-3  
Perfect score: 3615  
Sequence: 1 MTRPPGKAPASAPRAVRPG.....LAASIMLGVLTITLGLLVH 666

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1353	37.4	653	12 064906	Q64906 alcelaphine
2	810.5	22.4	612	12 09J5F6	Q9J5F6 fowlpox vir
3	680.5	18.8	893	4 Q9C0B8	Q9C0B8 homo sapien
4	617.5	17.1	748	4 Q8TB71	Q8TB71 homo sapien
5	601.5	16.6	754	4 Q8TDV7	Q8TDV7 homo sapien
6	597	16.5	756	13 Q8OGU9	Q8OGU9 gallus gall
7	596.5	16.5	635	4 Q96GX0	Q96GX0 homo sapien
8	566	15.7	775	11 Q9QX23	Q9QX23 mus musculu
9	534	14.8	782	4 Q9NS98	Q9NS98 homo sapien
10	516	14.3	761	4 Q8WUA9	Q8WUA9 homo sapien
11	500.5	13.8	963	4 Q9C0C4	Q9C0C4 homo sapien
12	444.5	12.3	1049	4 Q9P2H9	Q9P2H9 homo sapien
13	437	12.1	1030	4 Q9H2E6	Q9H2E6 homo sapien
14	426.5	11.8	296	11 Q9J129	Q9J129 rattus norv
15	418	11.6	1202	4 Q9P283	Q9P283 homo sapien
16	407	11.3	724	5 Q9V7Q7	Q9V7Q7 drosophila

17	402	11.1	1005	11 Q9E071	Q9E071 mus musculu
18	397.5	11.0	616	5 Q9V7P8	Q9V7P8 drosophila
19	393.5	10.9	1022	4 Q9P249	Q9P249 homo sapien
20	392.5	10.9	963	11 Q91Y36	Q91Y36 mus musculu
21	389	10.8	770	5 Q44253	Q44253 drosophila
22	389	10.8	935	4 Q96JF8	Q96JF8 homo sapien
23	387	10.7	770	5 Q9V3M4	Q9V3M4 drosophila
24	380.5	10.5	409	12 Q8OMR4	Q8OMR4 cowpox viru
25	380.5	10.5	687	4 Q9BXR8	Q9BXR8 homo sapien
26	373.5	10.3	923	11 Q8RAU3	Q8RAU3 mus musculu
27	368	10.2	416	12 Q98VP6	Q98VP6 vaccinia vi
28	360.5	10.0	920	11 Q8RAU4	Q8RAU4 rattus norv
29	349.5	9.7	457	4 Q9HBR1	Q9HBR1 homo sapien
30	337	9.3	419	4 Q96JY9	Q96JY9 homo sapien
31	312	8.6	676	5 Q9TY54	Q9TY54 caenorhabdi
32	311	8.6	475	4 Q96FK5	Q96FK5 homo sapien
33	310.5	8.6	458	4 Q8WVP9	Q8WVP9 homo sapien
34	309.5	8.6	1083	5 Q9VTT0	Q9VTT0 drosophila
35	304.5	8.4	1081	5 Q9U631	Q9U631 drosophila
36	276.5	7.6	367	4 Q9HAH9	Q9HAH9 homo sapien
37	267.5	7.4	284	11 Q54948	Q54948 mus musculu
38	248.5	6.9	510	4 Q9NX92	Q9NX92 homo sapien
39	246	6.8	424	4 Q9NS35	Q9NS35 homo sapien
40	236.5	6.5	816	5 Q9Y4A7	Q9Y4A7 drosophila
41	236.5	6.5	2051	5 Q96682	Q96682 drosophila
42	236	6.5	1951	5 Q8TA58	Q8TA58 caenorhabdi
43	230	6.4	228	12 Q9JF56	Q9JF56 vaccinia vi
44	224.5	6.2	1944	5 Q9N375	Q9N375 caenorhabdi
45	215	5.9	1892	11 Q9QY40	Q9QY40 mus musculu

## ALIGNMENTS

## RESULT 1

ID Q64906 PRELIMINARY: PRT: 653 AA.

AC Q64906;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE Similar to GENBANK ACCESSION number I26081.  
OS Alcelaphine herpesvirus 1 (wildbeest herpesvirus).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae.  
OC Gammaherpesvirinae; Rhadinovirus.  
OX NCBI\_TaxID=35252;  
RN [1]  
RP  
RC STRAIN=C500;  
RX MEDLINE=97404659; PubMed=9049359;  
RT Ensser A., Fleckenstein B.;  
RL "Alcelaphine herpesvirus type 1 has a semaphorin-like gene";  
RL J. Gen. Virol. 76:1063-1067(1995).  
RN [2]  
RP  
RC STRAIN=C500;  
RX MEDLINE=97404659; PubMed=9261371;  
RT Ensser A., Pflanz R., Fleckenstein B.;  
RL "Primary structure of the alcelaphine herpesvirus 1 genome";  
RL J. Virol. 71:6517-6525(1997).  
RN [3]  
RP  
RC STRAIN=C500;  
RX Ensser A., Pflanz R., Fleckenstein B.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U18243; AAC54475.1; -  
DR EMBL: AF005370; AAC58054.1; -  
DR InterPro: IPR001627; Sema; I.  
DR Pfam: PF01403; Sema; I.  
SQ SEQUENCE. 653 AA; 73645 MW; 5C2816BD567E706E CRC64;

Query Match 37.4%; Score 1353; DB 12; Length 653;  
Best Local Similarity 45.9%; Pred. No. 5.6e-106;

Matches	277: Conservative	86: Mismatches	228: Indels	12: Gaps
Qy	22	PARLG-LPRLRLLLLMAAASAGHLFSGRIFVWKGHGVGDQVNDGQEPHTVLEH	80	
Db	45	PAAMGLGVCSIRLMLL-SAITAASRFIDKPRLLVNLTDGFGQHRF--GGPEPHTVLEH	102	
Qy	81	EGGSSSVWVGGRGVKLVLEDFPEGKNASVFTVNIIGSTKSGCLDKRDENYITLLERSEGI	140	
Db	103	SLNSDVSYYVGGNNITVLEDFEFAHSSANSTALLINTSTHNHNRLLSTSCENTITLLHNQDGL	162	
Qy	141	LACGTHARHPSCWNLVNGTVLPLGEMKRGAPRSPDENSILVEEGDEYVSTIRKQENKGI	200	
Db	163	LACGTHARHPSCWNLVNLTLTQLEPRKLGLAPSPSSGNVLEPDQNDVSTINLYKSLSGS	222	
Qy	201	PAEPRIRGSELTSPDTVQNPQEFIKATIVHDDQAVDDKITYFFREDNDNDKPEAPLANS	260	
Db	223	HKFRIRAGVELYTSPTAMHRQFQVQATAVHNKNESTDKITYFFEQNSHSDKQEPHTVLP	282	
Qy	261	RYAQLCRGDQGESSLVSYSKMTFLKMLVCSDAATNNKFNRLQDVYLLPDPGQWRDR	320	
Db	283	RYGVQCSSDPQGESSLVSYSKMTFLKARLACVDYDGRITNELQDIFIQWAPENSWEETL	342	
Qy	321	YVGVSNNPNVYAVGVCSYSGDIDYKFRSTSLGYHSLPLNPBGKLTDPQGLPMPETFGV	380	
Db	343	ITGLELSPNPNVAVGVCSYSGDIDYKFRSTSLGYHSLPLNPBGKLTDPQGLPMPETFGV	402	
Qy	381	ADRHEDVAORVEMPRGLKTLPLFHSKYHKYQKAVVHRMQASHGETF--HYLLYTTDNGTIRK	438	
Db	403	ADREYEVADRVYQKNNAMPRIIGSKITYTKLLVYRE--YGVVFMATIEYLLTIGTINI	460	
Qy	439	VVEBGEQHSFAPNIMEIOPFRRAALIQMSLDAEERKLYVSQWESQVPLDLCEYVG	498	
Db	461	YVREDSNSTLTNLINLEINPQKPAPIQNLIDNTNLKLYVSEWESVPLDLCSYGN	520	
Qy	499	GCHGCLMSRDPYCGMDQGCISIIYSERSVLOSINPAEP--HKESCPNPKDPKAPLQKVS	556	
Db	521	DCFSQFMSDPLCTMYNNNC---SPKQKRVSVETGGRANTLSBMCGDHAPVAVVHQVSI	577	
Qy	557	APNSKRYLSCPMESNRHATYSMRHKENVEDQSCERGHOSPCLIFIENTLAQOYGHYFCEAO	616	
Db	578	PLLSNYSYLSCPAVSNHADYFWTKDGFTEKRCVHTKHKDCILLIINSTATNGTHVCMK	637	
Qy	617	EGS 619		
Db	638	EDS 640		

RESULT 2

Q9J5F6 PRELIMINARY: PRT: 612 AA.

AC Q9J5F6: 09J5F6:

01-OCT-2000 (TREMblrel. 15, Created)

01-OCT-2000 (TREMblrel. 15, Last sequence update)

01-JUN-2002 (TREMblrel. 21, Last annotation update)

ORF FV047 semaphorin vaccinia A39R homolog.

GN FV047.

OS Fowlpox virus (FPV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Avipoxvirus.

OC NCBI\_TaxID=10261:

RM [1]

RM SEQUENCE FROM N.A.

RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.; MEDLINE=20193820; PubMed=10729156;

RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.; "The genome of fowlpox virus."

RT J. Virol. 74:3815-3831(2000).

RN [2]

RP SEQUENCE FROM N.A.

RP Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.; Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL, AF198100; AAF44391.1; ..

DR InterPro; IPR003659; Plexin-like.

DR InterPro; IPR002165; Plexin-repeat

DR	InterPro:	IPR001627;	Sema.
DR	Pfam:	PF01437;	PSI; 1.
DR	Pfam:	PF01403;	Sema; 1.
DR	SMART;	SM00423;	PSI; 1.
DR	SEQUENCE	612 AA;	69514 MW; 175D0D18BC274E23 CRC64;
 Query Match            22.4%; Score 810.5; DB 12; Length 612; Best Local Similarity   32.9%; Pred. No. 5,3e-60; Matches 199; Conservative 108; Mismatches 224; Indels 73; Gaps 24;			
QY	52	PRIFAWKGVGDQRYDEGQTE--PHTVLEHPEGGSSVWVGKGKVYLFDPEEGKNASV-	108
	:	: : : : : :	:
	:	: : : : : :	:
DB	24	PRV---KSKLTENNIEEFKYTKYMEDVAIYRFDCQTRILIGTNTVYVNTDKSNITVD	79
QY	109	-RTVINIGSRSGCLDKRCDCENTITLERSEGLLGCINARHPSCMNVLNVG--VPLG	164
DB	80	EESPNDVSTDSGA-----NYTTTGIDYDKILVCGINNSSPTGW-YINGTIKPEPTYG	130
QY	165	EMRGAPSPDENSLVLEEGDEVYSTIRKOENYNGKIPRRRIERGESELLYSDTVMQNDF	224
DB	131	--RGLSPESDYDTGLIVLDIKREITYSTIK--YSHLSFGFSRIVGPKVLYTSASTKKNKPF	186
QY	225	IKATIVHDQAADKIYYFFREDNDDKNPEALNSRAOQLCRGOOGGESSLVSXKNMF	284
DB	187	VHLVSIQETENSINDTYLTFQEE-----GMAKVSRCCKHDQGSGLSGSKMSTF	236
QY	285	LKAMLVCSDAANKNKNFNRLQDYFELLPDPSGQWRDPTRYGVFSNPNNYSAVCYISLGDIK	344
DB	237	LKSIMICED--LNVARPNYLAKDVVIKGPS--NETIIIGLFENMNTSAYCMEFRKDQION	292
QY	345	VERTSSLKGYH--SLPLNPAPKCLPDQDPIPETTOVADRHEPAQARYEPMPGLKTLPLFH	403
DB	293	NNTSPFLKGYSGGKVLSPVPGTCL--NNTSPDFTFEVIDLPELYGYVK--GDF--TFK	345
QY	404	SKYHQKAVAHNMQASHGETFH--VLVLTDPGRGTTHKVV--EPGEQHSFAFINMETOP	458
DB	346	TYYTTHIVINAVINYQHOKOVRYTFLLSTDGKHKKVUYEDG-----VINYIELTL	399
QY	459	FRRAAAIOTMSIDAERRKLKYSSOWEVSQVPDLICEVYGAGCHGLCMSRDPCYGMDGRC	518
DB	400	KQYPSPVALVLSDERSEKIFVSYNSTETELPLAFCHLGGCTDSCLLSRDPHCQWTINDC	459
QY	519	ISIYSERSVLDSINPAERHKCEPMRKPDQAPL-QKVSIALPSRYVLSCPMESRATATSW	577
DB	460	--VYGGEEKLKLODIYDPKNICSSSLIKREFFSKVVLLSSSYVLSCLPESHQANTYW	517
QY	578	RHKEN-VROSCPEHQSPNCILFIENLTAOQYGHFYCEAEOGSGYFREAOHQMLPEDSIM	636
DB	518	VKKHKTIVDGGPRDN-NDMCWCFEYIYNLVDDNMGKYTCTSEEG-----WN---KETVM	565
QY	637	AHL 640	
DB	566	IHL 569	
 RESULT 3 Q9COB8 PRELIMINARY: PRT: 893 AA. AC Q9COB8: DT 01-JUN-2001 (TREMBLrel. 17, Created) DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update) DT 01-JUN-2002 (TREMBLrel. 21, Last annotation updates) DE KIA1745 protein (Fragment). GN KIA1745. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI_Taxid=9606; RN [1] RP SEQUENCE FROM N.A. RX MEDLINE=210829332; PubMed=11214970; RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XIX."			

RT The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.  
RL DNA Res. 7:347-355(2000).  
DR EMBL: AB051532; BAB21836.1; -  
DR InterPro: IPR003659; Plexin-like.  
DR InterPro: IPR002165; Plexin-like.  
DR Pfam: PF01437; PSI: 1.  
DR Pfam: PF01403; Sema: 1.  
DR SMART: SM00423; PSI: 1.  
FT NON\_TER  
SQ SEQUENCE 893 AA; 98361 MW; D6C6C48DEE524F14 CRC64;

Query Match 18.8%; Score 680.5; DB 4; Length 893;  
Best Local Similarity 30.1%; Pred. No. 9,8e-49;  
Matches 220; Conservative 89; Mismatches 293; Indels 129; Gaps 29;

4 PPGRAAPSAPRVRYPGPPA-----RLGL-----PLRLRLLL----- 37  
Db PVSPAEPEPEPEPDTVPALRLMTAMGLRSWLAAPGALPPRPRLLLLLLLQGP 94  
Qy 38 ---MAAASAGHLRSGRIFAVMKGHGQDRVDGTEPHTVLFHEGSSSVWVGGRK 94  
Db 95 PPTWALSRLPLGSESRPL-----RFEAHSNTALLSLRDGRTLYVGARBA 145  
Qy 95 ---LFDPECKNASVRTVNIKSTGSCLDK-----RDCENYI-TLLERRSEGLAC 143  
Db 146 LFAALLSNLSPFPGEGYOLMGADAEKKQCSFKGKDRQRCQNTIKILLPSSGHLTTC 205  
Qy 144 GTNARHPSGW--NLVNGTV-----VPLGEMRGYAPSPDENSLVLEEGDEVSTIRKQ 194  
Db 206 GTAAPSPCTIYIMENFTLAREKGNVLLDQKRCFPDPNFKSPALVVDGLY-TGVYS 264  
Qy 195 EYNGKIPFRKIRGSELSYTDV--MONPOFIKATYHOD-----QAVDKIYFFREDN 248  
Db 265 SFQGDPAFISQSILRPTKTESLMLQDPAFVASAYIPESIGSLQGDGDKYFFESSETEG 324  
Qy 249 PDKNEAPLANRYVAQLCRGDGGSSLSYSKWNFLKAMLYCSDAATNKNRLODFEL 308  
Db 325 QEFPEFENTYISRLARICKDGGGERVLD--QRTSFLKAQLCSKRPDGGFPENLVQDVFT 383  
Qy 309 LPDPSGQMDRTYVGVFSNPNY-----SAVCVSLGDIDYF-----RTSLKGY 354  
Db 384 LSPSPQMDRTLEGVFTSQWHRGTBEGSAVCFTMKDVORFESLYKEVNETQWYTV 443  
Qy 355 HSLSPNPPGCLPD--QQPIPTETFOYADR-----HEVAORVEPMGLKTP 401  
Db 444 THVPPTPRGACITNSAREKINSLSLQPLDRVLFKDHFLMDGQVRSRMLLOP----- 498  
Qy 402 FHSKYHGVAVHMQASHGETFHVLYLTDTGTHKVVYRGEDESHSAFNIMEIOPFR 461  
Db 499 ---QARYGVAVHVRPGH--HTYDVLFLGTGDRLHKAVSVGRPHI-----IEELQITSS 550  
Qy 462 AAATQMSLAERRKLYVSSQMEVSQVPLDCEVYGGGCHGLMSRDYCGMDQGRG--I 519  
Db 551 GQPVONLLDTHRGILYAASHGVQVPMANCSLY-RSCGOLLARDPYCAWSSGSKAHV 609  
Qy 520 SIYSE---RSVLQSIINAEPRKEC-----PNPKP-DKAPLQVSLAPNSRYLSCPM 568  
Db 610 SLVPOPLATRWIDIEGASAKDLCSASSVSPSPVPGEPCEDEVORQPMVNTLAPL 669  
Qy 569 ESRHATYSMRK---ENVEQSCPECHQSPNCILFENTLTAQOYGYFC-EAOGESYFREA 624  
Db 670 LSNLATRLMLKNGAPVNASASC---HYLPTGDDL--VGTQOLGEGQWSLEEGHQLVA 724  
Qy 625 QHMQLLPEDGI 635  
Db 725 SYCEPVEDGV 735

RESULT 4  
08TB71 PRELIMINARY; PRT; 748 AA.

AC Q8TB71:  
DT 01-JUN-2002 (TRENBLREL 21, Created)  
DT 01-JUN-2002 (TRENBLREL 21, Last sequence update)  
DT 01-JUN-2002 (TRENBLREL 21, Last annotation update)  
DE Hypothetical 83.0 kDa protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=MUSCLE;  
RA Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC024220; AAH24220.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 748 AA; 83034 MW; 587C53CB65AB4656 CRC64;

Query Match 17.1%; Score 617.5; DB 4; Length 748;  
Best Local Similarity 28.2%; Pred. No. 1.7e-43;  
Matches 202; Conservative 92; Mismatches 293; Indels 129; Gaps 27;

7 GRAAPSAPRVRYPGPPARLGLRLRLLLMA---AAASAGHLRSGRIFAVMKGHV 62  
Db 2 GRAGAAV---IPC-----LALLAVGLGSAAPRPRLRSLFQELQAMH--- 42  
Qy 63 GQDRVDGTEPHTVLFHEGSSSVWVGGRKVYLFDEPECKNASVRTVNI----- 113  
Db 43 GLQTFSLERTCCYQALVDEERGRLFVGAENIVASLNL---DNISKRAKKLAMPARVEMR 99  
Qy 114 -----GSTGSCLDKRCENYITLLERSE--GLACGTAHNPSCMNLVNGTVPLG-- 164  
Db 100 BECNAGKDIQT-----ECMNFVKLLHAYNTHLADGAGAHPTC-----AFEVGHR 148  
Qy 165 -----EMRGYAPSPDENSLVLEEGDEVSTIRKQYNGKIPFRIRGES 210  
Db 149 AEEPRLRLDPRGIEDGKGSPPYDRPHRAASVLYGCELYSGVAADLMGDFTFIRSLQRP 208  
Qy 211 ELYT---SDTYWQNOQFIKA--TIYQDOAYDDKIYFFREDNPKNPE--APLNVSRVAQL 265  
Db 209 SLRTPEHDSRMLNEPKPFKVFWEIPESNPDDKIEFFREFAVEAAPALGRLSRVQCI 268  
Qy 266 CRGDDGSSLSYSKWNFLKAMLYCS--DAATNKNRLODFELLPDPSGQMDRTYVYG 323  
Db 269 CRNDVGGORSL-VNKMWTFELKARLYCSVGYEGDTHFDQLDVFLL--SSRDHRTPLLYA 325  
Qy 324 VFSNP--MNSAVCVSLGDIDYF-----RTSLKGYHSLPMPRPGK----- 366  
Db 326 VESTSIFQGSAYCVYSNMVDYRAFLGPFARHKEGPMHQWVSQGVYPRPRQMCPSKTEG 385  
Qy 367 -LPDOOPIPTETFOYADHREVAORVEPMGLKTPF---HSKYHGVAVHMQASHGE 422  
Db 366 TFSSTKDEPDDVIOFARHNPMLYNSVLPFG--GRPLFQVQGANVYFTQIADRYAAAGH 443  
Qy 423 TEHVLYLTDTGTHKVVYRGEDESHSAFNIMEIOPFRRAAQTQMSLAERRKLYV 480  
Db 444 -YDVLEFGTGVTVLKVSVKGRSPSABGLLELHVFEDSAATYMQISSKRLQVYA 502  
Qy 481 SOMEVSQVPLDCEVYGGGCHGLMSRDYCGMDQRCISYSS--ERSVLQSIINAEPRH 538  
Db 503 SRSAVAQIALHRCAHGVCTECCCLARDPYCAMDQVACTRQPSAKRFRBRQVNGDPS 562  
Qy 539 KCPNPKDKAPLQ-KVSLAPNSRYLSCPMESRIATYSWRH-----KENVE 584  
Db 563 TILSGDSSRPALLERKVGVBGSSAFLECEPRSLQARVEMWFORAGVTAHTQVLAEBRTE 622  
Qy 585 OSCEPGHQSPNCILFENTLTAQOYGYFC-EAOGESYFREAQWMLLPEDGIASEHL 640  
Db 623 RTARG-----LLRLRLRRDSCVYLCAVAEGCFQPLRLSLHVIASQAEHL 670

RESULT 5  
08TDV7

ID Q8TDV7 PRELIMINARY; PRT: 754 AA.  
AC Q8TDV7;  
DT 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Semaphorin 3B.  
GN SEMA 3B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEMAPHORIN 3B (SEMA3B) CDNA."  
RA Koyama N.;  
RT "Semaphorin 3B (SEMA3B) CDNA."  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB083186; BAB88870.1; -  
SQ SEQUENCE 754 AA; 83691 MW; E61FD08C04E9A68E CRC64;

Query Match 16.6%; Score 601.5; DB 4; Length 754;  
Best Local Similarity 27.8%; Pred. No. 3.8e-42;  
Matches 201; Conservative 93; Mismatches 293; Indels 135; Gaps 28;

7 GRAPAPRARRVPPRRRLGLRLRLLLMA-----AASAGHLRSGRIFAWKCHV 62  
2 GRAGAAV---Tg-----LALLMAVGLGSAAPSPRLRLSTFELQAMH--- 42

63 GDRVDFGQEPHTVLFHEPGSSVWVGNGKYLFDPECKNASVTVNT----- 113  
43 GLQFSLERTCCYALLVDEGRGLFVGAENHVASLNL---DNISKRKKLAMPAPVEMR 99

114 -----GTSKGLDKDCENTITLERRSE-GLLAGCTNARHPSCMNLVNGTVPLG-- 164  
100 EECMAKDKDGT-----ECMNFVLLHAUYNTHLLAGCTGAFHPTC-----AEVEGHR 148

165 -----EMGYAFSPDENSLVLEEGDEVYSTRKQEVNGKIRFRIRGES 210  
149 AEEVVLALDPERIDGKSPYDRHRAASVLYGELYSAAADLMGRDPIIFISLQGR 208

211 ELYT---SDTYMNPQFIKA-TIVHDOQAVDKEYFEFREDNPKNPE-AELNVSRYAQL 265  
209 SLRTEPHDSRLNPEKFEKVMIPESENPDODKYFFERETAVEAARALGLTSVSRGQI 268

266 CRGQGGESSLSVSKMNTFLKAMLYCS--DAATKNFRNL-----QVYLLPDSGQGRD 318  
269 CRNDVGGQORSL-VKMTPEFLKARLVCSVPVEGDTHPDQLPRPAEDVTL--SSRHR 325

319 TRYGVGSPNP---WNYSAVCYSLGIDIKVF-----RTSSLKGYHSLPMPRGKC 366  
326 PLIYAVSTSSITFGSAVCYYSKMDYRRAFLGFAHKEGFMHGVSTYQGNVPTPRGMC 385

367 -----LPDQPIPTETFOVADNRHPEVAORFERMGLKTPLF--HSKYHYQVAVYHRM 416  
386 PSKTFGTFSSITKDRPDVYIOFARNHPLMYNSVLTPTG--GRPLFLQVANGVYFTQIADRV 443

417 QASIGEFHYLYLTDTGTHIKV--VEEGEHSFAFINIMEIOFRRRAAIAQYSLDAER 474  
444 AADG--YDVLFTGTDVGLKTVSVKGRSPSAEGLLELHVEFEDLSAATVSMQISSK 502

475 RKIVSSOWEVSQVPLDCEYVGGGCHGLMSRPYCGMDGRCISYSS--ERSVLOSI 532  
503 HOLYVASRAVAQIALRCANAGVCTECCIARDPYCAMDVACTROPSPAKRRFRRODV 562

533 NPAPRECEPNKPKDAPLQ-KVSLAPNSRYLLSCPMESRHATYSWRH----- 579  
563 RNDGPSTLSCGSDSSRPALLEKHYGVGESSAFLECEPRSLDARVEMFQORGATVANHQYL 622

580 -KENVEOSCEGHOSPNCLIFENLTAQOYGHYFCEAOEGSYFREAOHWOLLPDGIMAE 638  
623 AAEETERTARG-----LLRLRLRRDSGVLYCAAVEGFTQPLRLRLSLHVLASATQAE 674

639 HL 640

DB 675 RL 676

RESULT 6  
Q8GCU9 PRELIMINARY; PRT: 756 AA.  
AC Q8GCU9;  
DT 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Semaphorin 3F.  
GN SEMA3F.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEMAPHORIN 3F (SEMA3F) CDNA."  
RA Watanabe Y., Nakamura H.;  
RT "Axon guidance of the trochlear nerve by Sema 3F along mid-hindbrain boundary."  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB072930; BAB88691.1; -  
SQ SEQUENCE 756 AA; 85196 MW; C36754C02541EDB8 CRC64;

Query Match 16.5%; Score 597; DB 13; Length 756;  
Best Local Similarity 28.7%; Pred. No. 9.3e-42;  
Matches 202; Conservative 112; Mismatches 285; Indels 106; Gaps 33;

33 LLLMAAASAGHLNSGRPIFAWKCHVGDVDRG-----QEPHTVLFHEPGSSVW 88  
12 LLLTGMRAHKKD-VPTPRVQLSFELKATGAHFNFLNSSDYRLLLKDDHDMY 70

89 VGRGKYLFDPECKN-----ASVTVN--IGTSKGLDKDCENTITLLE--RR 136  
71 VGSMDYVSLDHLINERPLIHWPAQRIECLISKNS--NGEGNTRILQIPNR 127

137 SEGILAGCTNARHPSCMNLVNGTVV-----PLGEMRYAFSPDENSLVLEEGDE 186  
128 TH-LYVCGTAGVNPICAFINGRKAQDIIFYLEPDKLESGSKSYDPKVDVTSALINEE 186

187 VYSTIRKQEVNGKIRFRIRGESELYTSDTV-----MNPQFIKATV-HDOQAVDKEY 241  
187 LYAGV-YIDEGTDAIFRTMGKOTAMRTDQYNSRWLNDPAFVRAQLIPDSERNDDLY 245

242 YFFREDNPKNPEAPLN---SVRAOLCRGQGGESSLSVSKMNTFLKAMLYCS--DAA 295  
246 FFFRE---KSADAPLSGVYSRIGRICLNDGGHCL-VKMTPEFLKARLVCSVPBGD 300

296 TNKNFNRLQVFLLPDPSGQMRDR--VGVFS--NPNMYSAVCYSLGIDIKVFRT- 348  
301 IETHFELQDVEFI-----QOTQDTKPNPIYAVFASGVSFGSAVCYSMADIRVFNRP 355

349 -SSLKG-----YHSLPNRPGKC-----LPDQPIPTETFOVADNRHPEVAORVE 392  
356 FAHKEGPNYQMPPTGKMPYRPCTCGGTTPSKMSTKDPDEVINEMRSHPMYNAVY 415

393 PMGLKTPLF--HSKYHYQVAVYHRMDSHGEFFHYLYLTDTGTHIKV--VEEGEHS 448  
416 PAH--RQPLVRYTVNVRFTTIAVDQYDAADR-YEVLFTGTDGTYQKATVLEPRDKET 472

449 FAFNIMEIOFRRRAAIAQYSLDAERRKLYVSSOWEVSQVPLDCEYVGGGCHGLMSRD 508  
473 EELMLEIEVEKVPAPIKMNTISSKQQLYSSAVGTALHRCQVYGEACADCCCLARD 532

509 PYCGMDGRCISYSS--ERSVLOSIINPAEPHKEP--NPKPKAPLQKYSL-APNSRY 562  
533 PYCAMD-GKACRSYASASSKRSRQDVHGNPMQCGKYNANKNTVEAVOYVEGSTA 591

563 YLSCPMESRHATYSW-RHKEVNEOSCEGHOSPNCLIFENLTAQOYGHYFCEAO 616  
592 FLBCOPRSPQATVVKLLQKNSDRRKELRTEGRLALTEQGLLRALQLSDSGLYCTAT 651



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QY 500 CHGCLMSADPYCGMDGRCISLY-----SSERSVLQSLNPAEPHKECPNK--PDKAPLQ 552
D 526 CADCLADPYCAMDGISCSRYYPGTGAHAKRRFRQDVHNGNAOOCFGQCFVGDALDRT 585
QY 553 KVSILA---PNSRYLYSCSMESHRIATYSW-----RIKENVQ-----SCGEHGPSKCI 597
D 586 EERLALYGIESTLLECPTRSLQAKVIMFVOKGRDVRKEEVKTDDRVYKMDLG-----L 639
QY 598 LFIENTLTAQOYGHYFCEAOEGSY 620
D 640 LFL-RVRSKSDAGTYRCQTEVHNPF 661

RESULT 9
Q9NS98 PRELIMINARY: PRT: 782 AA.
ID Q9NS98
AC Q9NS98: Q9H703;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Semaphorin sem2 (FLJ00014 protein).
GN SEM2 OR FLJ00014.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Seki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Miyajima N.,
RT "Human semaphorin."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RC [2]
RC SEQUENCE OF 58-782 FROM N.A.
RC TISSUE=SPLEEN;
RA Ohara O., Nagase T., Kikuno R., Okumura K.;
RT "The nucleotide sequence of a long cDNA clone isolated from human
RT spleen."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB029496; BAA98132.1; -.
DR EMBL: AK024425; BAB15715.1; -.
DR InterPro: IPR003599; Iq_1-like.
DR InterPro: IPR003600; Iq_1-like.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003659; Plexin-like.
DR InterPro: IPR001627; Sema.
DR Pfam: PF00047; Iq_1.
DR Pfam: PF01403; Sema; 1.
DR SMART: SM00409; Iq; 1.
DR SMART: SM00410; Iq_1like; 1.
DR SMART: SM00423; PSI; 1.
SEQUENCE 782 AA; 86700 MW; 85CBA24874DF6663 CMC64;

Query Match 14.8%; Score 534; DB 4; Length 782;
Best Local Similarity 27.4%; Pred. NO. 2.2e-36;
Matches 194; Conservative 93; Mismatches 260; Indels 162; Gaps 33;

QY 4 PPPGAAPSARARVPGRPLRLRLLLMAAASA-----QGHLSGPRIFAVW 58
D 24 PSPG---PSVPRLR-----LSTRDL---SANKSALIFGPGSLNLOAMYLDY 66
QY 59 KGHV---GOD-----RVDFGOTEPHTLVF-HEPGSSVWVGKGVYLFDEPECKNASVR 109
D 67 RDRFLGLGLDALYSLRLQDAMPDPREVLPMPQPGQ----- 101
QY 110 TVNIGSTGSCLDK-----RDCENTILLERSE-GLIACGTNARHPSQWLVNVTYVPL 163
D 102 -----REECVRKGRDPLTECANFVYLOPHNRTHTLLACGGAPOPTCALI---TVGHR 151
QY 164 GEM-----RGVAPSPDENSILVFEGDEVYSTIRKQEVNGKIPRRIRIGSE 211
D 152 GEHVHLLEPGVESGKRCRPHPSRPFASPTIDGLTYGL-TADFLGREAMIFRSGGPRP 210
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QY 212 LYTSD---TWMCNPOFIKATIVHODAYD-DKIYFFREDNEKDPKPEALN---VSRAQ 264
D 211 ALRSDSDSLHDPREFVMAARIPENSDDONDKVYFFESFTEP--SPDGSNHVTVSRRGR 268
QY 265 ICRGQGGESSLSVSKNTFLKMLVCS---DAATNKFNRLQDVFLLPDPGQKRDIV 321
D 269 VCVNADGQORVL-VKWSFELFKARLVCSVPGPGAETHEDDQLEDFLLMPKAG--KSLEV 325
QY 322 YGVFSN---PMNYSAVCYVSLGIDIKVFR-----TSSLKGHSSLPNRPCKLPD 369
D 326 YALFSTVSAVFGFACVYHNADIMEVFNPRFANDGQROHQMGPIGKVPFRPQVC-PS 384
QY 370 Q---QP-----IPTEFGVADRHEVAGVPEMGP---LKTPLFHSKYHYQYAV 413
D 385 KWTAGPGRPGSTKDYRDEVLQFARAHPLMFVPVRPRHGRPALVTK---HLAQQLHQIYV 441
QY 414 HRMQASHGETFVLYLTDRGTIHKV--EPGEQESHAFNIMETQPRRAAIGTMSLD 471
D 442 DVEAEDG-TYDVIFLGTDSGSLVIALQAGSAPEEVLLEELQVKKVPPPIEMETS 500
QY 472 AERRKLTVSSQWESQVPLDCEVYGGGCHGCLMSRDPYCGMDGRCISIYSS---ERSV 528
D 501 VKRQMLYVSGRLGVAQLRHQCETGTACAECCLRDPLCAMDGASCTHYRSLGKRFR 560
QY 529 LOSINPAEPHKECPNPKDKAPLQKVSU---APNSRYLYSCSMESHRIATYSWRRKENY 583
D 561 RODIRHGNPDLQCLGSGDEEAVGLVATMYGTENSTFLECLPKSPQAAVRMLQ--- 617
QY 584 EDCSEPGHGPSNCI-----LFIENTLTAQOYGHYFCEAOEGSY 620
D 618 ---RPDGGEPQVKTDERVLTERTGLFRRLSRFDAGTYTCTTLEHGP 662
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RESULT 10
Q8WUA9 PRELIMINARY: PRT: 761 AA.
ID Q8WUA9
AC Q8WUA9;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 83.6 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC020974; AAB20974.1; -.
DR InterPro: IPR000005; HTHARAC.
DR InterPro: IPR003659; Plexin-like.
DR InterPro: IPR002165; Plexin-repeat.
DR InterPro: IPR001627; Sema.
DR Pfam: PF01437; PSI; 1.
DR Pfam: PF01403; Sema; 1.
DR SMART: SM00423; PSI; 1.
DR SMART: PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
KW Hypothetical protein.
SO SEQUENCE 761 AA; 83573 MW; 5BCB889AA32a2B83 CRC64;

Query Match 14.3%; Score 516; DB 4; Length 761;
Best Local Similarity 27.2%; Pred. NO. 7e-35;
Matches 204; Conservative 97; Mismatches 280; Indels 168; Gaps 36;

QY 21 PPARGLPL-RLRLLLMAAASAQGHLSRGRIFAVWKGHVQDRVDFGOTEPHTVL 78
D 10 PWSLGLFLFQLQLLPLTTTAGGGGQPM---PRV-----RYVADDERAALS-----F 55
QY 79 PHEPG-----SSVWVGKRGKGVYLFDF-----PECKN-----ASRYTVNIGST 116
```



OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRIN:  
RX MEDLINE=2018126; PubMed=10718198;  
RA Nagase T., Kikuno R., Ishikawa K., Hirosewa M., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XVI.  
RT The complete sequences of 150 new cDNA clones from brain which code  
RT for large proteins in vitro."  
RL DNA Res. 7:65-73(2000).  
DR EMBL: AB037789; BA92606.1;  
DR InterPro: IPR003659; Plexin-like.  
DR InterPro: IPR001627; Sema.  
DR Pfam: PF01403; Sema.  
DR SMART: SM00423; PSI: 1.  
FT NON\_TER 1  
SQ SEQUENCE 1049 AA; 116511 MW; 7781D20ACC7A8A6A CRC64;  
Query Match 12.3%; Score 444.5; DB 4; Length 1049;  
Best local Similarity 26.5%; Pred. No. 1.3e-28;  
Matches 162; Conservative 78; Mismatches 251; Indels 120; Gaps 27;  
DB 80 HEPG-----SSSVVGGRGKVVLFDEPECKNASV-----RTVN 112  
46 HKPGNTQRRHLDIOMIMNGTLYIAARDHIYVDIDTSTEEIYCSKLTWKSROAD 105  
113 IGSTGSCIDKRCENYI-TLLERSEGLACGTNARHPCSNLVNGTVPLG-EMRGYA 170  
106 VDTCKMKKHKHDECHNFKVLKKNDDALFVCGTNAFNSCNYMDTLEPGDEFGMA 165  
171 --PSPDENSILVFEEDVYS-----TIKQEVN--GKIPRRIRGESELYTSDTYM 219  
166 RCPYAKAHANVALFADGKLYSATVDFLAIDAVIYRSIGSEPTLRTVKHDSKW-----L 219  
220 QNPQIKATYHODAYDDKIYFFREDNPDKNPAFLNVSVAOLCRDGOESSLSYS 279  
220 KEPEVQAV-----DYGDIYFFFEIYAVENYNTGKVFPPVAVQCKNDMGSGRVLEK 273  
280 KWNFLKAMLYCS-DAATNKNENRLQDVFLLPDSQGMROTFRVYGVFSNPNVY---SAVC 335  
274 QMTSLKARLNCVSGDHFYFNILQAVTVIRING--RDV-VLATFTPTNYSIPGSAVC 330  
336 VYSLGIDIKVFTSLKGYHS-----SLPNPRGKC-----LPDQPIFTE 376  
331 AYDMIDLISVF-TGRFKKOKSPDSTWTVPDERVYKPRPGCCAGSSSLERYATSNEFPDD 389  
377 TFOVADRHREVAQRYEPMPGLKTPLE---HSKYHYQKVAVHRMQASHGETFHVLYLTDR 433  
390 TLNFKTHPLMDEAVPSI--FNRPWFELRTWRYRLTKLTAIVDTAGPY-QNHTVFLGSEK 446  
434 GTIHK-----VEPEGOEHSFAFNIMEIOFRRAA-----AIQTMSLDAERKLYVSQ 482  
447 GILKFLARINSGFLNLSLFLSEMSVYNSEKCSYDGEDKRIMQMDRASSSSLYAFS 506  
483 WEVSQVPLDCEVYGGGCHGLMSRDPYCGM--DQGRICISYSSRSVL-OSINAEPH- 538  
507 TCVIKVPLRGCEHKKCKKTCIASRDPYCGMIKEGACSHLSPNRLTFEODIEGNTDG 566  
539 -KECPN-----PKPDKAPLOKV-----SLAPNSRYLLSCP-----ESRHATYSWR 578  
567 LGDCHNSVALNDISTPLPDNEMSTNYVYGHSSSLPSTTTSDSTAQEGYESRGMGLDWK 626  
627 HLDSPTDTP 637  
RESULT 13  
ID 09H2E6 PRELIMINARY; PRT: 1030 AA.  
AC 09H2E6;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Semaphorin SEMA6A1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20564339; PubMed=1093894;  
RA Klostermann A., Lutz B., Gertler F., Behl C.;  
RT "The orthologous human and murine semaphorin 6A-1 proteins (SEMA6A-  
RT 1/SEMA6A-1) bind to the Enabled/Vasodilator-stimulated Phosphoprotein-  
RT like Protein (EVL) via a novel carboxyl-terminal zyxin-like domain."  
RL J. Biol. Chem. 275:39647-39653(2000).  
DR EMBL: AF279656; AAC29378.1;  
DR InterPro: IPR003659; Plexin-like.  
DR InterPro: IPR001627; Sema.  
DR Pfam: PF01403; Sema.  
DR SMART: SM00423; PSI: 1.  
SQ SEQUENCE 1030 AA; 114368 MW; A57B79C10AEC4B34 CRC64;  
Query Match 12.1%; Score 437; DB 4; Length 1030;  
Best local Similarity 26.1%; Pred. No. 5.4e-28;  
Matches 161; Conservative 80; Mismatches 251; Indels 126; Gaps 27;  
DB 80 HEPG-----SSSVVGGRGKVVLFDEPECKNASV-----RTVN 112  
44 HKPGNTQRRHLDIOMIMNGTLYIAARDHIYVDIDTSTEEIYCSKLTWKSROAD 103  
113 IGSTGSCIDKRCENYI-TLLERSEGLACGTNARHPCSNLVNGTVPLG-EMRGYA 170  
104 VDTCKMKKHKHDECHNFKVLKKNDDALFVCGTNAFNSCNYMDTLEPGDEFGMA 163  
171 --PSPDENSILVFEEDVYS-----TIKQEVN--GKIPRRIRGESELYTSDTYM 219  
164 RCPYAKAHANVALFADGKLYSATVDFLAIDAVIYRSIGSEPTLRTVKHDSKW-----L 217  
220 QNPQIKATYHODAYDDKIYFFREDNPDKNPAFLNVSVAOLCRDGOESSLSYS 279  
218 KEPEVQAV-----DYGDIYFFFEIYAVENYNTGKVFPPVAVQCKNDMGSGRVLEK 271  
280 KWNFLKAMLYCS-DAATNKNENRLQDVFLLPDSQGMROTFRVYGVFSNPNVY---SAVC 335  
272 QMTSLKARLNCVSGDHFYFNILQAVTVIRING--RDV-VLATFTPTNYSIPGSAVC 328  
336 VYSLGIDIKVFTSLKGYHS-----SLPNPRGKC-----LPDQPIFTE 376  
329 AYDMIDLISVF-TGRFKKOKSPDSTWTVPDERVYKPRPGCCAGSSSLERYATSNEFPDD 387  
377 TFOVADRHREVAQRYEPMPGLKTPLE---HSKYHYQKVAVHRMQASHGETFHVLYLTDR 433  
388 TLNFKTHPLMDEAVPSI--FNRPWFELRTWRYRLTKLTAIVDTAGPY-QNHTVFLGSEK 444  
434 GTIHK-----VEPEGOEHSFAFNIMEIOFRRAA-----AIQTMSLDAERKLYVSQ 482  
445 GILKFLARINSGFLNLSLFLSEMSVYNSEKCSYDGEDKRIMQMDRASSSSLYAFS 504  
483 WEVSQVPLDCEVYGGGCHGLMSRDPYCGM--DQGRICISYSSRSVL-OSINAEPH- 538  
505 TCVIKVPLRGCEHKKCKKTCIASRDPYCGMIKEGACSHLSPNRLTFEODIEGNTDG 564  
539 -KECPNPKPDKAPLOKVSLAPNSRYLLSCP-----MESRHATYSWRHKEVESC 587  
565 LGDCHN-----SFVALNGHSSSLPSTTTSDSTAQEGYESRGMGLDWKHLDSPTD 616  
588 EP-----GHOSPNCIL 598  
617 DPLGAVSSHNHODKKGVI 634  
RESULT 14  
ID 09J129





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